

STIC-Biotech/ChemLib

68880

Fr m: Scheiner, Laurie
Sent: Friday, June 14, 2002 10:56 PM
To: STIC-Biotech/ChemLib
Subject: seq. search request (09/808,212)

Please search SEQ ID NO:1 of application S.N. 09/808,212. Thanks!

Laurie Scheiner
Art Unit 1648
CM1 8E05
308-1122
8E12

RECEIVED
JUN 17 2002
STIC

if Contact:
Sheppard

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: 6/21/02
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST(where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

GenCore version 4.5
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OM nucleic - nucleic search, using sw model.

Run on: June 19, 2002, 16:25:56 ; Search time 1700.19 Seconds
(Without alignments)
1976.686 Million cell updates/sec

Title: US-09-808-212a-1
Perfect score: 249
Sequence: 1 atgaacatgaattgtctgtg.....ttaaattgtctgaataa 249

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 674847542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

EST.*
1: em_estdb.*
2: em_esthum.*
3: em_estin.*
4: em_estnu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hlc.*
9: gb_est1.*
10: gb_est2.*
11: gb_hlc.*
12: gb_gss.*
13: em_gss_hum.*
14: em_gss_inv.*
15: em_gss_pln.*
16: em_gss_vrt.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	24.9	602	12	AZ372526 IM0124L21
2	58.6	23.5	518	10	AZ771492 IM0573L10
3	58.2	23.4	318	10	BM159325 EST561848
4	57.6	23.1	475	10	BM029212 IPSkn0005
5	57.4	23.1	691	12	BH040136 RPCI-24-2
6	57.2	23.0	443	10	BM374465 EBP103_SO
7	57	22.9	379	10	BM164323 EST566846
8	57	22.9	380	10	BM162473 EST566996
9	57	22.9	559	10	BM165811 EST568334
10	57	22.9	608	10	BM163552 EST566075
11	55.8	22.4	715	10	BM170799 EST573322
12	55	22.1	550	10	BH264512 CH230-121
13	54.4	21.8	546	12	AZ600777 IM0418D18
14	54.4	21.8	596	12	AZ460541 IM0265124
15	54.2	21.8	481	10	BM441017 Ebed02_SQ
16	53.8	21.6	571	12	AO919110 RPCI-23-2
17	53.6	21.5	938	12	AZ676392 EMTW47TR

18	53.4	21.4	540	12	AZ813205
19	53.4	21.4	868	12	BH161951
20	53.2	21.4	725	12	BH180166
21	53	21.3	699	12	CNS03C21
22	53	21.3	718	12	CNS04PAC
23	53	21.3	878	12	AZ673988
24	53	21.3	970	12	BH137975
25	52.6	21.1	498	9	BE223146
26	52.6	21.1	976	12	AG136173
27	52.4	21.0	650	12	AZ722144
28	52.4	21.0	935	10	BE897269
29	51.8	20.8	421	12	AZ113646
30	51.8	20.8	865	12	AZ668061
31	51.8	20.8	917	12	BH148214
32	51.8	20.8	929	12	AZ688789
33	51.8	20.8	956	12	AZ167142
34	51.6	20.7	437	9	BE030214
35	51.6	20.7	476	10	BE579798
36	51.6	20.7	563	12	AZ026892
37	51.4	20.6	485	10	BM161844
38	51.4	20.6	861	12	AZ137643
39	51.2	20.6	382	12	BH043453
40	51.2	20.6	381	12	CNS010P2
41	51	20.5	326	9	BE223521
42	51	20.5	327	10	BE580799
43	51	20.5	330	10	BE580447
44	51	20.5	331	10	BG225320
45	51	20.5	333	10	BG224555

ALIGNMENTS

RESULT 1
AZ372526 602 bp DNA linear GSS 02-OCT-2000
LOCUS IM0124L21F Mouse 10kb plasmid UUC1M library Mus musculus genomic
DEFINITION clone UUC1M0124L21 F, DNA sequence.

ACCESSION AZ372526.1 GI:10486226

VERSION

KEYWORDS

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES
source

Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert length: 10000 Std Error: 0.00
Plate: 0124 row: 1, column: 21
Seq primer: CGTTGTAACGACGACGACG
Class: plasmid ends
High quality sequence stop: 602.
Location/Qualifiers
1. 602
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUC1M0124L21"
/clone_1lb="Mouse 10kb plasmid UUC1M library"

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT
84112, USA.

Tel.: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0573 row: L column: 10
Seq primer: CACACAGCAACACACTATGACC
Class: plasmid ends
High quality sequence stop: 518.
Location/Qualifiers
1. 518

FEATURES
Source

<http://www.jax.org/resources/documents/natnes/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMDA2 (g1147321141gb/AP129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin-resistance."

[illegible]

	RESULT	3			
	BMI59325				
LOCUS	BMI59325	318 bp	mRNA	linear	EST 04-DEC-2001
DEFINITION	EST561848 PYBS Plasmodium yoelli yoeiii cDNA clone pYCUGc2 5' end,				
	mRNA sequence.				
ACCESSION	BMI59325				
VERSION	BMI59325.1	GI:17305009			
KEYWORDS	EST.				
SOURCE	Plasmodium yoelli yoeiii.				
ORGANISM	Plasmodium yoelli yoeiii				

RESULT	4
BM029212	
LOCUS	BM029212 475 bp mRNA linear EST 05-NOV-2001
DEFINITION	Ipskno0051 skin cDNA library Ictalurus punctatus cDNA 5', mRNA sequence.

Russell, D.,

TITLE	JOURNAL	COMMENT
Mouse BAC End Sequences from Library RPCI-24	Unpublished (1999)	other_GSSs: RPCI-24-255A23.TJ

FEATURES	Location/Qualifiers
source	1. .691

RESULT	6
LOCUS	BM374465
DEFINITION	BM374465 443 bp mRNA linear EST 10-JAN-2002
ACCSSION	EBP103_S0003_L06_R IGF Barley EBP103 library Hordeum vulgare cDNA
VERSION	clone EBP103_S0003_L06_5' mRNA sequence.
KEYWORDS	BM374465
SOURCE	BM374465.1 GI:18117855
ORGANISM	EST.
	barley.
	Hordeum vulgare

TITLE	COMMENT
Development of Barley Transcriptome Resources Unpublished (2001) Contact: Waugh R.	

BASE COUNT	287 a	8 c	126 g	22 t
ORIGIN				

RESULT 7
 LOCUS BM164323
 DEFINITION BM164323 379 bp mRNA linear EST 04-DEC-2001
 ACCESSION E57566846 PyBS Plasmodium yoelii yoelii cDNA clone PCTL562 5' end,
 VERSION mRNA sequence.
 KEYWORDS BM164323.1 GI:17310004
 SOURCE EST.
 ORGANISM Plasmodium yoelii yoelii.
 Plasmodium yoelii yoelii.
 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 1 (bases 1 to 379).
 AUTHOR Carlton, J.M., Daly, T.M., Long, C.A., Bergman, L.W., Valdya, A.B.,
 Fraser, C.M. and Carnucci, D.J.
 TITLE Plasmodium yoelii EST project at TIGR
 JOURNAL Unpublished (2001)
 COMMENT Contact: Jane Carlton
 Parasite Genomics Group
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850, USA

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
1 (bases 1 to 559)
Carlton, J.M., Daly, T.M., Long, C.A., Bergman, L.W., Vaidya, A.B.,
Fraser, C.M. and Carucci, D.J.
Plasmodium yoelii: EST project at TIGR
Unpublished (2001)
Contact: Jane Carlton

FEATURES	Location/Qualifiers
source	1. .559

BASE COUNT	285 a	58 c	117 g	99 t
ORIGIN				

Query Match	22.9%;	Score 57;	DB 10;	Length 559;
Best Local Similarity	55.2%;	Pred. No. 0.77;		
Matches 11;	Conservative 0;	Mismatches 90;	Indels 0;	Gaps 0

Accession	Sequence	Position
OY	5 actttaaatttccttggaagaagaacacccaggaacacccaggaagacccaagaagaactta	64
Db	253 AATCAATTAAGGAGAGAGCAAGTCTTAAGAGAAACATAAAGAGAAACATAAGCAAGATT	312
OY	65 caatcaagaatttaacttaactcttgcaggttggaagatacaacagcagaattccaagaa	124
Db	313 AAGAGAGAGAAACAAAGAGAGCAAAAGAAAGAAAGCAAAAGAGAGAGCAACAGAGAG	372
OY	125 catttgaagaagcaacagcagaaagcttaacagatatgcagacttaattgcaaaagtaatg	184
Db	373 CAATGAAGCTGCAGAGAAAGCTGCAGAAAGCAAGCTGTAAAGAGAGCTGCAGAGAAAGCTTG	432
OY	185 ggaatatatacagcagacttag 205	
Db	433 CAGAGAGAGCTGCAATATGAG 453	

RESULT	10
BM163552	
LOCUS	
BM163552	608 bp mRNA
DEFINITION	linear
ES57566075	pyBS Plasmodium yoelli cdna clone pYLC59 5' end,
mRNA sequence.	

ACCESSION	BM163552	
VERSION	BM163552.1	GI:1730923
KEYWORDS	EST	
SOURCE	Plasmodium yoelii yoelii.	

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 608)	Carlton, V.M., Daly, T.M., Long, C.A., Bergman, L.W., Vaidya, A.B., Fraser, C.M. and Carnucci, D.J.	Plasmidome yoeIIi EST project at TIGR	Unpublished (2001)	Contact: Jane Carlton

FEATURES	Location/Qualifiers
source	1. 608

BASE COUNT	304 a	61 c	111 g	132 t
ORIGIN				

Query Match	22.9%;	Score 57;	DB 10;	Length 608;
Best Local Similarity	55.2%;	Pred. No. 0.76;		
Matches 111;	Conservative	0;	Mismatches 90;	Indels 0;
			Gaps	0;

QY 5 acatlaaatcttgcgaaagaacaccagaaacacccagaaagacccaaagaagaatla 64
Db 59 AAACAAGAGAGAAAGAAAGACTTAAAGAGAAACAAAGAGAAACAAAGAAAGACTTA 118
QY 65 caatcaagcttaacttaactcttgcagatggagaatgatacaacagcagcaattcaagaa 124
Db 119 AAGAGAGAGAGAAACAAAGAAAGACGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 178
QY 125 cattggaagaagcaacagcagagaagcttacagatattgcagacttaattgcaaaagtaatg 184
Db 179 CAAAGAAGCTGCAGAAAGACCTGCAGAAAGAGCTGTAAAGGAAGCTGCAGAAAGAACTTG 238
QY 185 gcaaatatagcagacttag 205
Db 239 CAGAAGAACTGCAGAAATGAG 259

OY	15	tcgtcgaaaagaataaccagaaacaccagaaagaccaaagaagaatgttcaatcaaatg	74
Db	234	tgaccacaaacaaatcagatgtaagaagaagatcaactgaaacaaaaaagaaattggaacact	293
OY	75	taacttaactcttcgagctggaagaatatacaaacagcagaaatctcaagaagaacttggaga	134
Db	294	tgagcaattagacaacacttgaaactgtrgaagtrgaalcaacaaattacaaagaaaaagaaacacc	353
OY	135	agcaacagcagaagcttacaatattgcagactttagcaaaagtaaatgtgcgaattac	194
Db	334	tgaacaaattacaaagagaagaaagaaatttgaaacacttgaaacaaattagaggtrgaacatgt	413

07 3 gaaccttaaatcttctgtgaaagaaccccgaaaccccgaaagaacccaagaagaat 62
Db 510 GAAAAAAGACAGACAGACAGACAGAAAGAAAGAAAGAACACACAGACAGACAGA 451
07 63 tacaatcgaagttaactaatcttgcagatggaagatcaaacagcgaatccaagg 122
Db 450 ACAAAGAAAGAAAGAAAGACAGACAGAAAGAAAGAACACACAGACAGACAGA 391
07 123 aacatttaagaagcaacgcgagaagcttacagatgacgactattagcaaaagtaa 182
Db 390 AGAAGAACAGACAGACAGACAGAAAGAAAGAAAGAACACACAGACAGACAGA 331

Oy 183 tgcgaatatatacagcagacttagaagatggttgaa 217
| | | | |
Db 330 AGAACAGAGAAGAGAAGAGAAGAAAGAGAGAA 296

RESULT	13
AZ600777/c	
LOCUS	546 bp DNA linear GSS 13-DEC-2000
DEFINITION	IM041BD18 Mouse 10kb plasmid U06C1M Library Mus musculus genomic clone U06C1M041BD18 R, DNA.sequence.

ACCESSION	A2600777
VERSION	A2600777.1
KEYWORDS	GSS.

SOURCE	house mouse.
ORGANISM	Mus musculus.

REFERENCE	1 (bases 1 to 546)
AUTHORS	Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Johnson, C., Johnson, M., Mooren, F., Pedersen, T., Relliv,

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
Center for the Study of the History of the

University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801/581-5506

Email: ddunn@genetics.utah.edu
Insert Length: 1000 Std Error: 0.00
Plate: 0418 row: D column: 18
Seq primer: CACACAGGAAACAGCATATGACC
Class: plasmid ends
High quality sequence stop: 546.

FEATURES	Location/Qualifiers
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 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UGCCIM0418D18"
 /clone.lib="Mouse 10kb plasmid UGCCIM library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMD42uv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/dnares/>). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 ligated DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of PMD42 (g11473211419b|AF129072.1), a copy number
 inducible derivative of plasmid R1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT
ORIGIN

Query Match	21.8%	Score	54.4	DB	12	length	546
Best Local Similarity	53.2%	Pred. No.	2.2				
Matches	115	Conservative	0	Mismatches	101	Indels	0
						Gaps	0

OY	19	ggaaaaaaacaccagaataccccaaggaaccaaaaagaaggttacaatcaagttaac	78
Db	544	GAAAGACGAAAGAAGAAAGAAAGAAAGAACAGACAGACAGAAAGAAAGAAAGAA	485
OY	79	ttaactcttgacagatgysnaagatcaaacagcagaaattcaaygaacatttgaagca	138
Db	484	GAAAGACGAAAGAAAAGAAAGAAAGAAAGAAAGACAGACAGAAAGAAAGAAAGAA	425
OY	139	acagcagaagcttacagatatgcagacttatagcaaaagfaaatgysnatatfacgca	198
Db	424	GAAGACGAAAGAAAGAAAGAAAGAAAGACAGACAGAAAGAAAGAAAGAAAGAA	365
OY	199	gacttagaagatgtgtgysnaaccatatgacaatta	234
Db	364	GACGACGAAAGAAAGAAAGAAATTAACAACCTTAA	329

RESULT	14				
A2460541					
LOCUS	A2460541	596 bp	DNA	linear	GSS 04-OCT-2000
DEFINITION	JM0265124R Mouse 10kb plasmid U06C1M library Mus musculus genomic				

ACCESSION	AZ460541	
VERSION	AZ460541.1	GI:106186666
KEYWORDS	GSS.	
SOURCE	house mouse.	

ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 596)
REFERENCE AUTHORS	Dunn,D., Aoyagi,A., Barber,M., Beacom,T., Faval,B., Hamill,C., Schwartz,W., Wenzel,H., Pedersen,T., Relliyil,J.

TITLE	Mouse whole genome scaffolding with paired end reads from 10xk
JOURNAL	plasmid inserts
COMMENT	unpublished (2000)
	Contact: Robert B. Weiss
	Genome Center

University of Utah:
Rm. 308, Biomedical Polymers Research Bldg.,
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0265 row: 1 column: 24
Seq Primer: CACACAGCAACAGCTATGACC
Class: Plasmid ends
High quality sequence stop: 556.

FEATURES
source

/organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U08C1M026512A"
 /clone_lib="Mouse 10kb plasmid U08C1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD42nv; Purified genomic DNA from Mus musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (q1443211419b) AF129072.1), a copy number

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 17:34:34 ; Search time 46.05 Seconds
(without alignments)
1328.181 Million cell updates/sec

Title: US-09-808-212A-1
Perfect score: 249
Sequence: 1 atgaacattaaatttgctg.....ttaattgctgaaataa 249

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/plodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/plodata/1/ina/6A_COMB.seq:*
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5: /cgn2_6/plodata/1/ina/PCUOS_COMB.seq:*
6: /cgn2_6/plodata/1/ina/backfill1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	231.4	92.9	876	US-08-446-137B-3
2	229.8	92.3	3279	US-08-446-137B-1
3	181.2	72.8	921	US-08-795-475-2
4	181.2	72.8	1308	US-08-795-475-4
5	109.8	44.1	548	US-08-828-741B-1
6	109.8	44.1	548	US-09-160-567-1
7	107	43.0	539	US-08-828-741B-12
8	107	43.0	539	US-09-160-567-12
9	107	43.0	599	US-08-828-741B-7
10	107	43.0	599	US-09-160-567-7
11	107	43.0	1031	US-08-828-741B-5
12	107	43.0	1031	US-09-160-567-5
13	107	43.0	1490	US-08-828-741B-3
14	107	43.0	1490	US-09-160-567-3
15	50.6	20.3	3337	US-08-072-610-1
16	50.6	20.3	3337	US-08-719-822B-1
17	50.6	20.3	3337	US-09-092-458-1
18	50.2	20.2	7218	US-08-232-463-14
19	50	20.1	2223	US-08-257-073-4
20	44	17.7	1320	US-08-257-073-15
21	44	17.7	1482	US-08-098-327E-41
22	44	17.7	1482	US-08-098-327E-45
23	44	17.7	1482	US-08-462-625-41
24	44	17.7	1482	US-08-462-625-45
25	44	17.7	1493	US-08-098-327E-38
26	44	17.7	1493	US-08-462-625-38
27	42.8	17.2	696	US-09-461-697-193

28	42.8	17.2	699	US-09-461-697-191	Sequence 191, App
29	42.8	17.2	717	US-09-461-697-189	Sequence 189, App
30	42.8	17.2	774	US-09-461-697-187	Sequence 187, App
31	42.8	17.2	819	US-09-461-697-185	Sequence 185, App
32	42.8	17.2	1699	US-09-461-697-184	Sequence 184, App
33	42	16.9	864	US-08-858-207A-132	Sequence 132, App
34	41	16.5	289	US-09-007-005-17	Sequence 17, App
35	41	16.5	289	US-09-244-796-17	Sequence 17, App
36	41	16.5	397	US-09-253-691-3	Sequence 3, App
37	40.8	16.4	231	US-09-461-697-207	Sequence 207, App
38	40.8	16.4	282	US-09-461-697-205	Sequence 205, App
39	40.8	16.4	306	US-09-461-697-203	Sequence 203, App
40	40.4	16.2	5361	US-08-973-462-2	Sequence 2, App
41	40.4	16.2	6152	US-08-973-462-1	Sequence 1, App
42	40.2	16.1	213	US-09-461-697-209	Sequence 209, App
43	40	16.1	1276	US-08-628-417-6	Sequence 6, App
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45	39.8	16.0	1276	US-09-411-812A-2	Sequence 2, App

ALIGNMENTS

RESULT 1
US-08-446-137B-3
Sequence 3, Application US/08446137B
Patent No. 6162903
GENERAL INFORMATION:
APPLICANT: Trowern, Angus R.
APPLICANT: Atkinson, Anthony
APPLICANT: Murphy, Jonathan P.
APPLICANT: Laurence, Oliver S.
APPLICANT: Dugleby, Clive J.
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEINS DERIVED FROM L PROTEIN AND THEIR USES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446.137B
FILING DATE: 22-MAY-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 100084.406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 876 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: *Peptostreptococcus*
STRAIN: 1018
FEATURE:

NAME/KEY: CDS
LOCATION: 1..876
US-08-446-137B-3

Query Match 92.9%; Score 231.4; DB 4; Length 876;
Best Local Similarity 95.6%; Pred. No. 1.7e-47;
Matches 238; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

OY 1 atgaacattaaattgctggaagaaacacacaggaagaaacacaaagaaga 60
DB 628 ATCAACATTAAATTGCTGGAAGAAACACACAGAAACACGAGAAACCAAAAGAA 687
OY 61 gttaacataaagtaacttaattcttgagatggaagatacaaacagcagaattcaa 120
DB 688 GTTACATCAAGTTAAGTTAATCTTGCAGATGMAAACACAAACAGCAAGATTCAAA 747
OY 121 ggaacattggaagaagcaagcagaagcttcagatatagcagacttttagcaaaagta 180
DB 748 GGAAACATTTGAAGAGAACACACAGAAAGCTTACAGATATGACAGACTTATTACCAAAAGTA 807
OY 181 aatggcgaatatatacagcagacttagaagatggtggaacataatgaacattatgct 240
DB 808 AATGGTGATACACAGACAGACTTAGAAGATGGCGATACACTATCAACATCAAAATTGCT 867
OY 241 ggaataata 249
DB 868 GGAATAATA 876

RESULT 2
US-08-446-137B-1
Sequence 1, Application US/08446137B

Patent No. 6162903
GENERAL INFORMATION:

APPLICANT: Tiwerton, Angus R.
APPLICANT: Atkinson, Anthony
APPLICANT: Murphy, Jonathan P.
APPLICANT: Laurence, Oliver S.
APPLICANT: Dugdaley, Clive J.
TITLE OF INVENTION: IMMUNOGLOBULIN BINDING PROTEINS DERIVED
TITLE OF INVENTION: FROM L PROTEIN AND THEIR USES
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446/137B
FILING DATE: 22-MAY-1995
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Mcmasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 100094.406
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3279 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Peptostreptococcus asaccharolyticus
STRAIN: 1018
FEATURE:
NAME/KEY: exon
LOCATION: 103..3186

IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /codon_start=280
OTHER INFORMATION: /product="mature protein L"
OTHER INFORMATION: /evidence=EXPERIMENTAL
OTHER INFORMATION: /number=1

NAME/KEY: CDS
LOCATION: 103..3186
OTHER INFORMATION: /codon_start=103
OTHER INFORMATION: /product="Immature protein L"
FEATURE:
NAME/KEY: mat.peptide
LOCATION: 280..3183
OTHER INFORMATION: /codon_start=280
OTHER INFORMATION: /product="mature protein L"

FEATURE:
NAME/KEY: misc.signal
LOCATION: 208..279
US-08-446-137B-1

Query Match 92.3%; Score 229.8; DB 4; Length 3279;
Best Local Similarity 95.2%; Pred. No. 5.4e-47;
Matches 237; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

OY 1 atgaacattaaattgctggaagaaacacacaggaagaaacacaaagaaga 60
DB 1576 ATCAACATTAAATTGCTGGAAGAAACACACAGAAACACGAGAAACCAAAAGAA 1635
OY 61 gttaacataaagtaacttaattcttgagatggaagatacaaacagcagaattcaa 120
DB 1636 GTTACATCAAGTTAAGTTAATCTTGCAGATGMAAACACAAACAGCAAGATTCAAA 1695
OY 121 ggaacattggaagaagcaagcagaagcttcagatatagcagacttttagcaaaagta 180
DB 1696 GGAAACATTTGAAGAGAACACACAGAAAGCTTACAGATATGACAGACTTATTACCAAAAGTA 1755
OY 181 aatggcgaatatatacagcagacttagaagatggtggaacataatgaacattatgct 240
DB 1756 AATGGTGATACACAGACAGACTTAGAAGATGGCGATACACTATCAACATCAAAATTGCT 1815
OY 241 ggaataata 249
DB 1816 GGAATAATA 1824

RESULT 3
US-08-795-475-2
Sequence 2, Application US/08795475

GENERAL INFORMATION:
APPLICANT: Bjvick, Lars
APPLICANT: Sjvding, Ulf
TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,475
FILING DATE: 11-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McMASTERS, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 100084.40201
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 921 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Escherichia coli LE392/PHDL, DSM 7054
US-08-795-475-2

Query Match 72.8%; Score 181.2; DB 2; Length 921;
Best Local Similarity 86.3%; Pred. No. 1.9e-35;
Matches 214; Conservative 0; Mismatches 28; Indels 6; Gaps 1;

OY 2 tgaacattaaatttgcgtgaaagaacacccagaacacccaagaagaagaagaag 61
DB 653 TAAATATTAAATTTCTGTAAGAAA-----AAACACCAAGAACCAAAAGAAAG 706
OY 62 ttacatcaagttacttaattcttgcagatggaagatacaaacagcagaattcaag 121
DB 707 TTACTATTAAAGCAAACTTAATCTATGCAATGCAAAAACTCAACACAGAGTTCAAG 766
OY 122 gaacattggaagaagcagaagcagaagcttacagatgacagactattagcaagaagta 181
DB 767 GAACATTTGCAGAACCAACAGCAGATACAGATACGCTGACTTATTAGCAAAAGAA 826
OY 182 atgagcaatatacagcagacttagaagatggtggaacacatagacattaaattgctg 241
DB 827 ATGTAATAATATACACAGACTTAGAAGATGCTGATACACTTAAATATTGATTGCGAG 886
OY 242 gaaataa 249
DB 887 GTAAGAAA 894

RESULT 4
US-08-795-475-4
Sequence 4, Application US/08795475
Patent No. 5965390

GENERAL INFORMATION:
APPLICANT: Bjvick, Lars
APPLICANT: Sjøvding, Ulf
TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,475
FILING DATE: 11-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: McMASTERS, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 100084.40201
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1308 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Escherichia coli L392/PHDLG, DSM 7055
US-08-795-475-4

Query Match 72.8%; Score 181.2; DB 2; Length 1308;
Best Local Similarity 86.3%; Pred. No. 2.1e-35;
Matches 214; Conservative 0; Mismatches 28; Indels 6; Gaps 1;

OY 2 tgaacattaaatttgcgtgaaagaacacccagaacacccaagaagaagaagaag 61
DB 653 TAAATATTAAATTTCTGTAAGAAA-----AAACACCAAGAACCAAAAGAAAG 706
OY 62 ttacatcaagttacttaattcttgcagatggaagatacaaacagcagaattcaag 121
DB 707 TTACTATTAAAGCAAACTTAATCTATGCAATGCAAAAACTCAACACAGAGTTCAAG 766
OY 122 gaacattggaagaagcagaagcagaagcttacagatgacagactattagcaagaagta 181
DB 767 GAACATTTGCAGAACCAACAGCAGATACAGATACGCTGACTTATTAGCAAAAGAA 826
OY 182 atgagcaatatacagcagacttagaagatggtggaacacatagacattaaattgctg 241
DB 827 ATGTAATAATATACACAGACTTAGAAGATGCTGATACACTTAAATATTGATTGCGAG 886
OY 242 gaaataa 249
DB 887 GTAAGAAA 894

RESULT 5
US-08-828-741B-1
Sequence 1, Application US/08828741B
Patent No. 6043069

GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Suenes, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,741B
FILING DATE: 26-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Digilio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4366
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 548 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..548
US-08-828-741B-1

Query Match 44.1%; Score 109.8; DB 3; Length 548;
Best Local Similarity 68.0%; Pred. No. 2.5e-18;
Matches 153; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
DB 25 gaacaccagaacaccagaagacacaaagaagattacaattcaacttaattc 84
52 GTAGCGAGGCGCGCTCGAAGATTAACGAGAGAGTACGATCAAGGACGACCTGATC 111
QY 85 ttgtgagatgaaagatatacaacagcagaatttaagaacatttaagaagaacagca 144
DB 112 TTTCGAATAGTGACACACAACTGCAAGATTAAGATCTTCGAAAAAGCGACCTCG 171
QY 145 gaagcttaagatagcagactattagcaaaagtaaatgycgaatatatacagcagactta 204
DB 172 GAAGCTTAAGCTTAAGCAGATCTTGAAGAGAGACAAATGCGAATATCTGATGATGTT 231
QY 205 gaagatggtgaaacacatatagaacataatttgcgtgaaataa 249
DB 232 GCAGATTAAGGTTACACCTGAAACATCAAAATTCGCGGTTAAAGAA 276

RESULT 6
US-09-160-567-1
Sequence 1, Application US/09160567
Patent No. 6326179
GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
City: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,567
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,741
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Digilio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4366
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 548 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..548
US-09-160-567-1

Query Match 44.1%; Score 109.8; DB 4; Length 548;
Best Local Similarity 68.0%; Pred. No. 2.5e-18;
Matches 153; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
DB 25 gaacaccagaacaccagaagacacaaagaagattacaattcaacttaattc 84
52 GTAGCGAGGCGCGCTCGAAGATTAACGAGAGAGTACGATCAAGGACGACCTGATC 111
QY 85 ttgtgagatgaaagatatacaacagcagaatttaagaacatttgaagaagacagca 144
DB 112 TTTCGAATAGTGACACACAACTGCAAGATTAAGATCTTCGAAAAAGCGACCTCG 171
QY 145 gaagcttaagatagcagactattagcaaaagtaaatgycgaatatatacagcagactta 204
DB 172 GAAGCTTAAGCTTAAGCAGATCTTGAAGAGAGACAAATGCGAATATCTGATGATGTT 231
QY 205 gaagatggtgaaacacatatagaacataatttgcgtgaaataa 249
DB 232 GCAGATTAAGGTTACACCTGAAACATCAAAATTCGCGGTTAAAGAA 276

RESULT 7
US-08-828-741B-12
Sequence 12, Application US/08828741B
Patent No. 6043069
GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
City: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,741B
FILING DATE: 26-MAR-1997

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SRO ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 539 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..539
US-08-828-741B-12

Query Match 43.08; Score 107; DB 3; Length 539;
Best Local Similarity 71.88; Pred. No. 1.2e-17;
Matches 140; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY 55 gaagaatttaacatcaagtttaacttaactcttcagatggaagaatatacacaagcagaa 114
DB 34 GAAGAAGTCACGATCAAAAGCGAACCTGATCTTTCGAATGTTAGCAGACACAACTGCAGAA 93
QY 115 ttcaagaagaacatttgaagaagaacagcagaagcttacagatatgcagacttattaga 174
DB 94 TTCAAGGTACTCTCGAAAAAGCGACCTCGAGAGCTTATGCGTATGCGATGACTTTGAG 153
QY 175 aaagtaaatgacgatatacagcagacttgaagaatgltggaaccatatagaacattaa 234
DB 154 AAAGACATGCTGATGATGCTAGTAGATGTCAGATTAAGGTTACACCTGAACATCMAA 213
QY 235 ttctctgaaataa 249
DB 214 TTCCGGGGTAAGAA 228

RESULT 8
US-09-160-567-12
Sequence 12, Application US/09160567
Patent No. 6326179
GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,567
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,741

FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SRO ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 539 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..539
US-09-160-567-12

Query Match 43.08; Score 107; DB 4; Length 539;
Best Local Similarity 71.88; Pred. No. 1.2e-17;
Matches 140; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY 55 gaagaatttaacatcaagtttaacttaactcttcagatggaagaatatacacaagcagaa 114
DB 34 GAAGAAGTCACGATCAAAAGCGAACCTGATCTTTCGAATGTTAGCAGACACAACTGCAGAA 93
QY 115 ttcaagaagaacatttgaagaagaacagcagaagcttacagatatgcagacttattaga 174
DB 94 TTCAAGGTACTCTCGAAAAAGCGACCTCGAGAGCTTATGCGTATGCGATGACTTTGAG 153
QY 175 aaagtaaatgacgatatacagcagacttgaagaatgltggaaccatatagaacattaa 234
DB 154 AAAGACATGCTGATGATGCTAGTAGATGTCAGATTAAGGTTACACCTGAACATCMAA 213
QY 235 ttctctgaaataa 249
DB 214 TTCCGGGGTAAGAA 228

RESULT 9
US-08-828-741B-7
Sequence 7, Application US/08828741B
Patent No. 6043069
GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,741B
FILING DATE: 26-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.

RESULT 10
 US-09-160-567-7
 : Sequence 7, Application US/09160567
 Patent No. 6326179
 GENERAL INFORMATION:
 APPLICANT: Koentgen, Frank
 APPLICANT: Suess, Gabriele M.
 APPLICANT: Tarlinton, David M.
 APPLICANT: Treutlein, Herbert R.
 TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
 TITLE OF INVENTION: PRODUCING SAME
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: SULLIVY, SCOTT, MURPHY & PRESSER
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: New York
 COUNTRY: United States of America
 ZIP: 11530
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/160,567
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/828,741
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Digiglio, Frank S

RESULT 11
US-08-828-741B-5
Sequence 5, Application US/08828741B
Patent No. 6043069
GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Suess, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treulhorn, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
City: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,741B
FILING DATE: 26-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: DigiGlo, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1031 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1031
US-08-828-741B-5

Query Match 43.0%; Score 107; DB 3; Length 1031;
Best Local Similarity 66.0%; Pred. No. 1.3e-17;
Matches 155; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

Qy 15 tgcctggaagaagacacacagagaacacagagaacacagagaagttacatcaagt 74
Db 486 TGGTGTGTCGCAAAACCTGCTACTTCAGGGTGTAAGCCCGAAGAGTCACGATCAAGC 545
Qy 75 taacttaattcttgcagatggaagatatacaacagcagaaattcaaaagacattgga 134
Db 546 GAACCTGATCTTTGCAAAATGTTAGCAGACACAACTGCAGAAATTCAAAGTACTCTGAAA 605
Qy 135 agcaacagcagaagcttcagatatgcagacttattagcaaaagtaaatgacgaataac 194
Db 606 AGCGACCTCGGAGAGCTTATGCGTATGCAAGATCTTTGAAGAAAGCAATGCTGATATAC 665
Qy 195 agcagacttaagaatgltggaacacataatgaacattaaatttctggaataa 249
Db 666 TGTAGATGTGCAGATTAAGGTTACACCTGTAACATCAAAATTCGGGGTAAGAA 720

RESULT 12

US-09-160-567-5
Sequence 5, Application US/09160567
Patent No. 6326179

GENERAL INFORMATION:

APPLICANT: Koentgen, Frank
APPLICANT: Sues, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,567
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/828,741
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1031 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1031
US-09-160-567-5

Query Match 43.0%; Score 107; DB 4; Length 1031;
Best Local Similarity 66.0%; Pred. No. 1.3e-17;
Matches 155; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

Qy 15 tgcctggaagaagacacacagagaacacagagaacacagagaagttacatcaagt 74
Db 486 TGGTGTGTCGCAAAACCTGCTACTTCAGGGTGTAAGCCCGAAGAGTCACGATCAAGC 545
Qy 75 taacttaattcttgcagatggaagatatacaacagcagaaattcaaaagacattgga 134
Db 546 GAACCTGATCTTTGCAAAATGTTAGCAGACACAACTGCAGAAATTCAAAGTACTCTGAAA 605
Qy 135 agcaacagcagaagcttcagatatgcagacttattagcaaaagtaaatgacgaataac 194
Db 606 AGCGACCTCGGAGAGCTTATGCGTATGCAAGATCTTTGAAGAAAGCAATGCTGATATAC 665
Qy 195 agcagacttaagaatgltggaacacataatgaacattaaatttctggaataa 249
Db 666 TGTAGATGTGCAGATTAAGGTTACACCTGTAACATCAAAATTCGGGGTAAGAA 720

RESULT 13

US-08-828-741B-3
Sequence 3, Application US/08828741B
Patent No. 6043069

GENERAL INFORMATION:

APPLICANT: Koentgen, Frank
APPLICANT: Sues, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,741B
FILING DATE: 26-MAR-1997
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR

GENERAL INFORMATION:
APPLICANT: Koentgen, Frank
APPLICANT: Sness, Gabriele M.
APPLICANT: Tarlinton, David M.
APPLICANT: Treutlein, Herbert R.
TITLE OF INVENTION: CATALYTIC ANTIBODIES AND A METHOD OF
TITLE OF INVENTION: PRODUCING SAME
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SCULLY, SCOTT, MORPHY & PRESSER
STREET: 400 garden city plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/160,567
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/828,741
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 10591
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR

GENERAL INFORMATION:
APPLICANT: Barnwell, John
TITLE OF INVENTION: Plasmodium vivax Blood Stage Antigens,
TITLE OF INVENTION: Monoclonal Antibodies, and Diagnostic Assays
TITLE OF INVENTION: Monoclonal Antibodies, and Diagnostic Assays
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby and Darby
STREET: 805 Third Ave.
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10022-7513
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/072,610
FILING DATE: 19930602
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gogoris, Adda
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 5986/07686
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)527-7700
TELEFAX: (212)753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3337 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear

Thu Jun 20 13:15:23 2002

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 17:38:59 ; Search time 214.27 Seconds
(without alignments)
1995.201 Million cell updates/sec

Title: US-09-808-212a-1
Perfect score: 249
Sequence: 1 atgaacataaattgtctgtg.....ttaattgtcgtgaaataa 249

Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 segs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_032802:*

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2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
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13: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:*
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22: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	249	100.0	249	AAA08425	Ig light chain bin
2	245.8	98.7	249	AAA08443	PPL mutant nucleot
3	244.2	98.1	249	AAA08442	PPL mutant nucleot
4	244.2	98.1	249	AAA08445	PPL mutant nucleot
5	241	96.8	249	AAA08444	PPL mutant nucleot
6	231.4	92.9	876	AA050947	Immunoglobulin bin
7	229.8	92.3	3279	AA050946	Sequence encoding
8	229.8	92.3	3279	AA051536	Sequence encoding
9	209	83.9	225	AAA08433	Peptostreptococcus

ID	Score	Query Match	Length	ID	Description
10	204.4	82.1	222	AAA08432	Peptostreptococcus
11	191.8	77.0	213	AAA08431	Peptostreptococcus
12	181.2	72.8	921	AA050452	Sequence encoding
13	181.2	72.8	1305	AA084644	Profilin-GDPex encod
14	181.2	72.8	1305	AA084644	Nucleotide sequenc
15	181.2	72.8	1305	AA084644	Sequence encoding
16	181.2	72.8	1308	AA050453	Nucleotide sequenc
17	171.8	69.0	216	AA084730	Peptostreptococcus
18	166.4	66.8	216	AA084730	Peptostreptococcus
19	156.8	63.0	216	AA084730	Peptostreptococcus
20	136.4	54.8	228	AAA08426	Peptostreptococcus
21	127.2	51.1	213	AAA08430	Peptostreptococcus
22	109.8	44.1	548	AA084590	Growth factor LHL
23	109.8	44.1	539	AA084591	Growth factor LHL
24	107	43.0	539	AA084591	Growth factor LHL
25	107	43.0	539	AA084591	Growth factor LHL
26	107	43.0	539	AA084591	Growth factor LHL
27	107	43.0	539	AA084591	Growth factor LHL
28	107	43.0	1031	AA084592	Growth factor LHL
29	107	43.0	1031	AA084592	Growth factor LHL
30	107	43.0	1479	AA084596	Growth factor LHL
31	107	43.0	1490	AA084597	Growth factor LHL
32	107	43.0	1490	AA084591	Growth factor LHL
33	86.2	34.6	6094	AA084591	Growth factor LHL
34	58.6	23.5	1686	AA084591	Growth factor LHL
35	56	22.5	379	AA084591	Growth factor LHL
36	56	22.5	379	AA084591	Growth factor LHL
37	56	22.5	3399	AA084591	Growth factor LHL
38	56	22.5	3399	AA084591	Growth factor LHL
39	53.2	21.4	1407	AA084591	Growth factor LHL
40	52.8	21.2	29392	AA084591	Growth factor LHL
41	51.4	20.6	483	AA084591	Growth factor LHL
42	51.2	20.6	1167	AA084591	Growth factor LHL
43	50.6	20.3	3337	AA084591	Growth factor LHL
44	50.6	20.3	3337	AA084591	Growth factor LHL
45	50.6	20.3	3337	AA084591	Growth factor LHL

ALIGNMENTS

RESULT 1

AAA08425 standard; DNA: 249 BP.

AAA08425:

20-JUL-2000 (first entry)

Ig light chain binding protein PPL construct DNA sequence SPQ ID NO:1.

Immunoglobulin light chain binding protein: PPL; protein L;

Peptostreptococcus; human immunoglobulin kappa chain;

Immunofluorescence chromatography; ds.

Peptostreptococcus sp.

WO200015803-A1.

23-MAR-2000.

14-SEP-1999; 99WO-GB03048.

14-SEP-1998; 98GB-0019998.

26-APR-1999; 99GB-0009578.

(ACTIN) ACTINOVA LTD.

Gore MG, Beckingham JA, Roberts SE;

WPI: 2000-271441/23.

P-PSDB: AAY82536.

PT New modified immunoglobulin light chain binding protein, useful in
PT immunofluorescence chromatography, has a dissociation constant of 400 nM or
PT more at pH8 with respect to human immunoglobulin kappa-chain
XX
XX
PS Claim 1; Page 38-39; 56pp; English.

XX The present invention describes an immunoglobulin (Ig) light chain
CC binding protein (PI) which has been modified by one or more amino acid
CC substitutions such that the dissociation constant (Kd) of the protein
CC with respect to human Ig kappa-chain is 400 nM or more at pH8. PI is
CC useful in immunofluorescence chromatography. The present sequence encodes an
CC Ig light chain binding PPL construct derived from Peptostreptococcus sp.
CC protein L.
XX

SO Sequence 249 BP; 116 A; 36 C; 47 G; 50 T; 0 other;

Query Match 100.0%; Score 249; DB 21; Length 249;
Best Local Similarity 100.0%; Pred. No. 6e-45;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atgaacatttaattgtgtgaaagaaagaaacccagaaacccagaaagaaagaaagaa 60
DB 1 atgaacatttaattgtgtgaaagaaagaaacccagaaacccagaaagaaagaaagaa 60
QY 61 gttaacatcaagtttaacttaattcttgcagatggaagatatacaacagagaattcaaa 120
DB 61 gttaacatcaagtttaacttaattcttgcagatggaagatatacaacagagaattcaaa 120
QY 121 ggaacatttgaagaagacagacagagcttacagatatcagactattatagaacaaagta 180
DB 121 ggaacatttgaagaagacagacagagcttacagatatcagactattatagaacaaagta 180
QY 181 aatgagcgaatatacagcagacttagaagatggtgaaacacatatagaacatttaattgct 240
DB 181 aatgagcgaatatacagcagacttagaagatggtgaaacacatatagaacatttaattgct 240
QY 241 ggaataataa 249
DB 241 ggaataataa 249

RESULT 2

AAA08443
ID AAA08443 standard; DNA; 249 BP.

XX
AC AAA08443;

DT 20-JUL-2000 (first entry)

XX PPL mutant nucleotide sequence SEQ ID NO:20

XX Immunoglobulin light chain binding protein; PPL; protein L;
KW Peptostreptococcus; human immunoglobulin kappa chain; mutant;
KW immunofluorescence chromatography; site directed mutagenesis; ds.
XX
OS Peptostreptococcus sp.

XX
PN WO200015803-A1.

XX
PD 23-MAR-2000.

XX
PF 14-SEP-1999; 99WO-GB03048.

XX
PR 14-SEP-1998; 98GB-0019998.

XX
PR 26-APR-1999; 99GB-0009578.

XX
PA (ACTI-) ACTINOVA LTD.

XX
PI Gore MG, Beckingham JA, Roberts SE;

XX
DR WPI; 2000-271441/23.

XX
DR P-PSDB; AAY82546.

XX
PT New modified immunoglobulin light chain binding protein, useful in
PT immunofluorescence chromatography, has a dissociation constant of 400 nM or
PT more at pH8 with respect to human immunoglobulin kappa-chain
XX
XX
PS Example 1; Page 51; 56pp; English.

XX The present invention describes an immunoglobulin (Ig) light chain
CC binding protein (PI) which has been modified by one or more amino acid
CC substitutions such that the dissociation constant (Kd) of the protein
CC with respect to human Ig kappa-chain is 400 nM or more at pH8. PI is
CC useful in immunofluorescence chromatography. The present sequence encodes a
CC mutant Peptostreptococcus protein L, which is an Ig light chain binding
CC protein, from the present invention.
XX

SO Sequence 249 BP; 117 A; 37 C; 47 G; 48 T; 0 other;

Query Match 98.7%; Score 245.8; DB 21; Length 249;
Best Local Similarity 99.2%; Pred. No. 2.9e-44;
Matches 247; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 atgaacatttaattgtgtgaaagaaagaaacccagaaacccagaaagaaagaaagaa 60
DB 1 atgaacatttaattgtgtgaaagaaagaaacccagaaacccagaaagaaagaaagaa 60
QY 61 gttaacatcaagtttaacttaattcttgcagatggaagatatacaacagagaattcaaa 120
DB 61 gttaacatcaagtttaacttaattcttgcagatggaagatatacaacagagaattcaaa 120
QY 121 ggaacatttgaagaagacagacagagcttacagatatcagactattatagaacaaagta 180
DB 121 ggaacatttgaagaagacagacagagcttacagatatcagactattatagaacaaagta 180
QY 181 aatgagcgaatatacagcagacttagaagatggtgaaacacatatagaacatttaattgct 240
DB 181 aatgagcgaatatacagcagacttagaagatggtgaaacacatatagaacatttaattgct 240
QY 241 ggaataataa 249
DB 241 ggaataataa 249

RESULT 3

AAA08442
ID AAA08442 standard; DNA; 249 BP.

XX
AC AAA08442;

DT 20-JUL-2000 (first entry)

XX PPL mutant nucleotide sequence SEQ ID NO:19.

XX Immunoglobulin light chain binding protein; PPL; protein L;
KW Peptostreptococcus; human immunoglobulin kappa chain; mutant;
KW immunofluorescence chromatography; site directed mutagenesis; ds.
XX
OS Peptostreptococcus sp.

XX
PN WO200015803-A1.

XX
PD 23-MAR-2000.

XX
PF 14-SEP-1999; 99WO-GB03048.

XX
PR 14-SEP-1998; 98GB-0019998.

XX
PR 26-APR-1999; 99GB-0009578.

XX
PA (ACTI-) ACTINOVA LTD.

XX
PI Gore MG, Beckingham JA, Roberts SE;

XX
DR WPI; 2000-271441/23.

DR P-PSDB; AAY82545.
XX New modified immunoglobulin light chain binding protein, useful in
PT immunofinity chromatography, has a dissociation constant of 400 nM or
PT more at pH8 with respect to human immunoglobulin kappa-chain -
XX
XX Example 1; Page 50-51; 56pp; English.
PS
XX The present invention describes an immunoglobulin (Ig) light chain
CC binding protein (PI) which has been modified by one or more amino acid
CC substitutions such that the dissociation constant (Kd) of the protein
CC with respect to human Ig kappa-chain is 400 nM or more at pH8. PI is
CC useful in immunofinity chromatography. The present sequence encodes a
CC mutant Peptostreptococcus protein L, which is an Ig light chain binding
CC protein, from the present invention.
XX
SQ Sequence 249 BP; 117 A; 36 C; 47 G; 49 T; 0 other;

Query Match 98.1%; Score 244.2; DB 21; Length 249;
Best Local Similarity 98.8%; Pred. No. 6.5e-44;
Matches 246; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 atgaacattaaatttctggaagaacaccagaaacacagaaagaaacaaagaaga 60
Db 1 atgaacattaaatttctggaagaacaccagaaacacagaaagaaacaaagaaga 60
QY 61 gttaacatcaaatgtaacttaattcttgcagatggaagatacaaacagcagaattcaa 120
Db 61 gttaacatcaaatgtaacttaattcttgcagatggaagatacaaacagcagaattcaa 120
QY 121 ggaacatttgaagaagacagacagaaagcttacagatatgagacttattgcaaaagta 180
Db 121 ggaacatttgaagaagacagacagaaagcttacagatatgagacttattgcaaaagta 180
QY 181 aatggcgaatatatacagcagacttagaagatggtggaacacatagacattaaatttgc 240
Db 181 aatggcgaatatatacagcagacttagaagatggtggaacacatagacattaaatttgc 240
QY 241 ggaataataa 249
Db 241 ggaataataa 249

RESULT 4

AAA08445
ID AAA08445 standard; DNA: 249 BP.

AC AAA08445;

DT 20-JUL-2000 (first entry)

DE Ppl mutant nucleotide sequence SEQ ID NO:22.

XX Immunoglobulin light chain binding protein; Ppl; protein L;

KW Peptostreptococcus; human immunoglobulin kappa chain; mutant;

KM immunofinity chromatography; site directed mutagenesis; ds.

XX Peptostreptococcus sp.

OS

PN WO200015803-A1.

PD 23-MAR-2000.

PF 14-SEP-1999; 99WO-GB03048.

PR 14-SEP-1998; 98GB-0019998.

PR 26-APR-1999; 99GB-0009578.

XX (ACTI-) ACTINOA LTD.

XX Gore MG, Beckingham JA, Roberts SE;

DR WPI; 2000-271441/23.
DR P-PSDB; AAY82548.
XX New modified immunoglobulin light chain binding protein, useful in
PT immunofinity chromatography, has a dissociation constant of 400 nM or
PT more at pH8 with respect to human immunoglobulin kappa-chain -
XX
XX Example 1; Page 53; 56pp; English.
PS
XX The present invention describes an immunoglobulin (Ig) light chain
CC binding protein (PI) which has been modified by one or more amino acid
CC substitutions such that the dissociation constant (Kd) of the protein
CC with respect to human Ig kappa-chain is 400 nM or more at pH8. PI is
CC useful in immunofinity chromatography. The present sequence encodes a
CC mutant Peptostreptococcus protein L, which is an Ig light chain binding
CC protein, from the present invention.
XX
SQ Sequence 249 BP; 116 A; 37 C; 47 G; 49 T; 0 other;

Query Match 98.1%; Score 244.2; DB 21; Length 249;
Best Local Similarity 98.8%; Pred. No. 6.5e-44;
Matches 246; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 atgaacattaaatttctggaagaacaccagaaacacagaaagaaacaaagaaga 60
Db 1 atgaacattaaatttctggaagaacaccagaaacacagaaagaaacaaagaaga 60
QY 61 gttaacatcaaatgtaacttaattcttgcagatggaagatacaaacagcagaattcaa 120
Db 61 gttaacatcaaatgtaacttaattcttgcagatggaagatacaaacagcagaattcaa 120
QY 121 ggaacatttgaagaagacagacagaaagcttacagatatgagacttattgcaaaagta 180
Db 121 ggaacatttgaagaagacagacagaaagcttacagatatgagacttattgcaaaagta 180
QY 181 aatggcgaatatatacagcagacttagaagatggtggaacacatagacattaaatttgc 240
Db 181 aatggcgaatatatacagcagacttagaagatggtggaacacatagacattaaatttgc 240
QY 241 ggaataataa 249
Db 241 ggaataataa 249

RESULT 5

AAA08444
ID AAA08444 standard; DNA: 249 BP.

AC AAA08444;

DT 20-JUL-2000 (first entry)

DE Ppl mutant nucleotide sequence SEQ ID NO:21.

XX Immunoglobulin light chain binding protein; Ppl; protein L;

KW Peptostreptococcus; human immunoglobulin kappa chain; mutant;

KM immunofinity chromatography; site directed mutagenesis; ds.

XX Peptostreptococcus sp.

OS

PN WO200015803-A1.

PD 23-MAR-2000.

PF 14-SEP-1999; 99WO-GB03048.

PR 14-SEP-1998; 98GB-0019998.

PR 26-APR-1999; 99GB-0009578.

XX (ACTI-) ACTINOA LTD.

XX Gore MG, Beckingham JA, Roberts SE;

OS Peptococcus magnus.

XX Key Location/Qualifiers

FT CDS 103..3185

FT /*tag= a

FT /product= Protein L.

FT repeat_unit 490..573

FT /*tag= b

FT /note= "Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide positions 673 and 856"

FT repeat_unit 574..672

FT /*tag= c

FT /note= "Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide position 757"

FT repeat_unit 949..1044

FT /*tag= d

FT /note= "Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide positions 1162, 1375 and 1597"

FT repeat_unit 1045..1158

FT /*tag= e

FT /note= "Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide positions 1261, 1483 and 1705"

FT repeat_unit 1822..1938

FT /*tag= f

FT /note= "Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide positions 2347, 2545 and 2731"

FT repeat_unit 2914..2934

FT /*tag= g

FT /note= "Repeat units are adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide positions 2935, 2953, 2968, 2986, 3001, 3019 and 3034"

XX WO9322439-A.

XX PD 11-NOV-1993.

XX PF 07-MAY-1993; 93WO-GB00950.

XX PR 07-MAY-1992; 92GB-0009804.

XX PR 24-DEC-1992; 92GB-0026928.

XX PA (PUBL-) PUBLIC HEALTH LAB SERVICE BOARD.

XX PI Atkinson A, Duggleby CJ, Murphy JP, Trowern AR.

XX DR WPI; 1993-368798/46.

XX DR P-PSDB; AAR42203.

XX PT New immunoglobulin binding proteins derived from Protein L - which bind immunoglobulin kappa light chains but not albumin or cell walls

XX PS Disclosure; Figure 1; 28pp; English.

XX CC The synthetic immunoglobulin binding proteins derived from protein L comprise repeated sequences from protein L which bind immunoglobulin kappa light chains. They can be used in protein analysis, purification procedures and other biochemical processes e.g. ELISA. The synthetic molecules are of particular advantage if they are free of regions in protein L which exhibit albumin and cell wall binding (the repeat regions commencing at nucleotide numbers 1045, 1261, 1483 and 1705).

XX Sequence 3279 BP; 1505 A; 481 C; 625 G; 668 T; 0 other;

Query Match 92.3%; Score 229.8; DB 14; Length 3279;

Best Local Similarity 95.2%; Pred. No. 1.1e-40;

Matches 237; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

QY 1 atgaacattaatttgcggaaagaaacacacagaaacagaaacccaagaaga 60

DB 1576 atcaacattaatttgcggaaagaaacacacagaaacagaaacccaagaaga 1635

QY 61 gtacaacaaagtaacttaattcttgcagatggaaagatacaacgcagaaatcaa 120

DB 1636 gtacaacaaagtaacttaattcttgcagatggaaagatacaacgcagaaatcaa 1695

QY 121 ggaacattgaaagcagacagcagaaagcttacagatgcaactattgcaaaagta 180

DB 1696 ggaacattgaaagcagacagcagaaagcttacagatgcaactattgcaaaagta 1755

QY 181 aatgcgaatatcacagcagacttagaagatggtgaaacccatgaacattaattgct 240

DB 1756 aatggtgatacacagcagacttagaagatggtgatacactatacaacattaattgct 1815

QY 241 ggaataata 249

DB 1816 ggaataata 1824

RESULT 8

AA051556

ID AA051556 standard; CDNA; 3279 BP.

XX AC AA051556;

XX DT 18-MAY-1994 (first entry)

XX DE Sequence encoding protein L.

XX KW Protein; immunoglobulin; binding; immobilisation; light chains;

XX KW antibodies; diagnosis; pharmaceutical; ss.

XX OS Peptococcus magnus.

XX Key Location/Qualifiers

FT CDS 103..3185

FT /*tag= a

FT /product= Protein L.

FT repeat_unit 490..573

FT /*tag= b

FT /note= "Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide positions 673 and 856"

FT repeat_unit 574..672

FT /*tag= c

FT /note= "Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide position 757"

FT repeat_unit 949..1044

FT /*tag= d

FT /note= "Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide positions 1162, 1375 and 1597"

FT repeat_unit 1045..1158

FT /*tag= e

FT /note= "Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide positions 1261, 1483 and 1705"

FT repeat_unit 1822..1938

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FT /note= "Repeat units are not adjacent, repetitions of this sequence are not 100% homologous and begin at nucleotide positions 2347 and 2545"

Sequence 222 BP; 105 A; 35 C; 40 G; 42 T; 0 other;

RESULT 11
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Sequence 213 BP; 100 A; 32 C; 40 G; 41 T; 0 other;

XX
AC AAQ50

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RESULT 12
AAQ50452
ID AAQ50452 standard; DNA; 921 BP
XX
AC AAQ50452;

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cc
XX
WITHOUT LOSS OF ACTIVITY.

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 16:35:23 ; Search time 1834.72 Seconds
(without alignments)
2840.056 Million cell updates/sec

Title: US-09-808-212a-1
Perfect score: 249
Sequence: 1 atgacataaattgtctg.....ttaattgtctggaataaa 249

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 segs, 10463268293 residues
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Listing first 45 summaries

Database: GenEmbl:
1: gb_ba:*
2: gb_htg:*
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5: gb_ov:*
6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
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23: em_pat:*
24: em_ph:*
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33: em_htgo_in:*

Pred.-No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Query Score Match Length DB ID Description

1	231.4	92.9	876	6	AR137037	AR137037 Sequence
2	230.4	92.5	876	6	A75725	A75725 Sequence 3
3	229.8	92.3	3258	1	PEPROMEIN	L04466 ReproStrept
4	229.8	92.3	3279	6	A75723	A75723 Sequence 1
5	229.8	92.3	3279	6	A75727	A75727 Sequence 1
6	229.8	92.3	3279	6	AR137036	AR137036 Sequence
7	181.2	72.8	921	6	AR079000	AR079000 Sequence
8	181.2	72.8	1308	6	AR079001	AR079001 Sequence
9	181.2	72.8	1365	1	S50809	S50809 Protein Ig-
10	181.2	72.8	2657	1	PEPPEPTIN	M86677 Pepostrept
11	109.8	44.1	548	6	AX022441	AX022441 Sequence
12	109.8	44.1	548	6	AX030798	AX030798 Sequence
13	109.8	44.1	548	6	AX034619	AX034619 Sequence
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15	107	43.0	539	6	AX030809	AX030809 Sequence
16	107	43.0	539	6	AX034628	AX034628 Sequence
17	107	43.0	539	6	AX022447	AX022447 Sequence
18	107	43.0	599	6	AX022447	AX022447 Sequence
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25	107	43.0	1490	6	AX030800	AX030800 Sequence
26	107	43.0	1490	6	AX034621	AX034621 Sequence
27	86.2	34.6	6094	6	AX027906	AX027906 Sequence
28	86.2	34.6	6094	12	AX027912	AX027912 Sequence
29	65.8	26.4	167227	9	AC020602	AC020602 Homo sapi
30	62.4	25.1	159587	2	AC098547	AC098547 Rattus no
31	62.4	25.1	169048	2	AC106675	AC106675 Rattus no
32	61.8	24.8	212411	2	AC099645	AC099645 Mus muscu
33	60.8	24.4	199508	2	AC098555	AC098555 Rattus no
34	60.4	24.3	208006	2	AC087877	AC087877 Mus muscu
35	59.8	24.0	215352	2	AC101119	AC101119 Mus muscu
36	59.8	24.0	215352	2	AC007305	AC007305 Mus muscu
37	59.4	23.9	71123	2	AC103643	AC103643 Mus muscu
38	59.2	23.8	205252	2	AC098460	AC098460 Rattus no
39	59.2	23.8	220820	2	AL653060	AL653060 Mus muscu
40	58.6	23.5	631	3	PEPPEK51	X53026 P. falciparu
41	58.6	23.5	1686	23	E08995	E08995 DNA encodin
42	58.6	23.5	150193	2	AC106120	AC106120 Rattus no
43	58.2	23.4	165675	9	AC090646	AC090646 Homo sapi
44	58.2	23.4	166466	2	AC095476	AC095476 Rattus no
45	58.2	23.4	166991	9	AC090884	AC090884 Homo sapi

ALIGNMENTS

RESULT 1
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LOCUS AR137037 876 bp DNA
DEFINITION Sequence 3 from patent US 6162903.
ACCESSION AR137037
VERSION AR137037.1 GI:14478287
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 876)
AUTHORS Trowern,A.R., Atkinson,A., Murphy,J.P., Laurence,O.S. and
Dugdaley,C.J.
TITLE Immunoglobulin binding proteins derived from L protein and their
uses
JOURNAL Patent: US 6162903-A 3 19-DEC-2000;
FEATURES
source location/Qualifiers
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BASE COUNT 402 a 141 c 162 g 171 t
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/rpt_type=direct
/evidence=experimental
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/evidence=experimental
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2035..2208
/note="2 E-repeats E1 (2035-2208) E2 (2209-2346); putative; E-repeats"
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2914..3051
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/function="charged cell anchor"
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3052..3183
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BASE COUNT 1495 a 477 c 623 g 663 t
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Matches 237; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 1 atgacacattaaattgctggaagaacacacagaaacacagaaacacaaagaaga 60
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Db 1576 ATCAACATTAAATTGCTGGAAAAGAACACACAGAACACACAGAACAGAA 1635
QY 61 gtacacatcaagtaacttaattcttgcagatggaagatacaacagcagaattcaaa 120
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Db 1636 GTTACAAATTAATTGCTGGAAAAGAACACACAGAACACACAGAACAGAA 1635
QY 121 ggaacattggaagaacagcagaagcttacagatatgagaattatgacaaagta 180
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Db 1696 GGAACATTTGAAAGAACAGACAGAAAGCTTACAGATATGACAGACTTATTGCAAAAGTA 1755
QY 181 aatggcgaatatagacagacttagaagatggtggaacacatgaacatlaattgct 240
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Db 1756 AATGGTGAATACACAGACAGACTTAGAAGATGCGGATACACTATCAACATCAAAATTGCT 1815
QY 241 ggaataca 249
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Db 1816 GGAAGAGAA 1824

RESULT 4
A75723 3279 bp DNA linear PAT 22-OCT-1999
LOCUS A75723
DEFINITION Sequence 1 from Patent WO93322439.
ACCESSION A75723
VERSION A75723.1 GI:6065694
KEYWORDS
SOURCE Peptostreptococcus sp. 1018.
ORGANISM Peptostreptococcus sp. 1018.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
peptostreptococcus.
REFERENCE 1 (bases 1 to 3279)
AUTHORS Trowern,A.R. and Atkinson,A.
TITLE IMMUNOGLOBULIN BINDING PROTEINS DERIVED FROM L PROTEIN AND THEIR

JOURNAL USES
Patent: WO 9322439-A 1 11-NOV-1993;
HEALTH LAB SERVICE BOARD (GB); TROWERN ANGUS ROBERT (GB)
FEATURES
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TAKEBAEKLAAREKAKRHIDSLNLSETAKRLANDISATTNAINDIVARADVM
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Best Local Similarity 95.2%; Pred. No. 5.2e-33;
Matches 237; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 1 atgacacattaaattgctggaagaacacacagaaacacagaaacacaaagaaga 60
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Db 1576 ATCAACATTAAATTGCTGGAAAAGAACACACAGAACACACAGAACAGAA 1635
QY 61 gtacacatcaagtaacttaattcttgcagatggaagatacaacagcagaattcaaa 120
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Db 1636 GTTACAAATTAATTGCTGGAAAAGAACACACAGAACACACAGAACAGAA 1635
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QY 241 ggaataca 249
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Db 1816 GGAAGAGAA 1824

RESULT 5
A75727 3279 bp DNA linear PAT 22-OCT-1999
LOCUS A75727
DEFINITION Sequence 1 from Patent WO93322438.
ACCESSION A75727

[illegible][illegible]

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QY	62	ttacaatcaaaagttaacttaactcttttcagatgtaagaagatatacaaacagcagaattc	121
Db	707	TTACATTATTAAGCAACAACCTTAATCTATGACAGATGAGAAAACCTAAACAGCAGAGTTCAAG	766
QY	122	gaacatttgaagaagcaaacagcagaagctttacagatatgcagacttattagcaaaagtaa	181
Db	767	GAACATTTTGCAGAACCAACAGACAGAGCATACAGATAGCGCTGATTTATTAGCAAAAGAAA	826
QY	182	atggcgaatatatcacgcagaacttagaagatggtggaacacatatgacattaaatttgc	241
Db	837	ATGGTAATTAATAACACCAACTTAGAAGATGGTGATACACTAATTAATTTAGATTTCAG	886
QY	242	gaaaataa 249	
Db	887	GTAAGAA 894	

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DEFINITION	AR079001	1308 bp	DNA	linear	
ACCESSION	AR079001	Sequence 4 from patent US 5965390.			
VERSION	AR079001.1	GI:10005747			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	1 (bases 1 to 1308)				
AUTHORS	Bjorck,L. and Sjobring,U.				
TITLE	Protein L and hybrid proteins thereof				
JOURNAL	Patent: US 5965390-A 4 12-OCR-1999;				
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OY	62	ttacaatcaaaagttacttaatcctttgcagatgtaagaatatacaaacagcagaatccaag	121	
Db	707	TTACTATTAAAGCAACACTTAATCTATGCAAGATGAGAAAAAAGCTAAACACGACGAGTTCAAG	766	
OY	122	gaacctttgaaagaacacacagcagaagccttaagatatgacagacttataggaaaagtaa	181	
Db	767	GAAACATTTGCAAGAACCAACGACGAAGCATTAACAGATACCGCTACTTATTATGCAAAAAGAA	826	
OY	182	atgsgaatatcacagcagacttagaagatgtygtgaaacccatatagcaactlaaatctgctg	241	
Db	827	ATGCGTAAATATATCACACAGACTTAGAAGATGCTGATACACTATTATATATTAACTTTGCG	886	
OY	242	gaaataa	249	
Db	887	GTAAGAA	894	

LOCUS	S50809	1365 bp	mRNA	linear	BCT-02-MAR-2001
DEFINITION	protein LG-immunoglobulin binding protein [immunoglobulin binding domains] [streptococcus, mRNA Recombinant], 1365 nt.				
ACCESSION	S50809				
VERSION	S50809.1	GI:261705			
KEYWORDS					
SOURCE	Finegoldia magna.				
ORGANISM	Finegoldia magna Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae; Finegoldia. 1 (bases 1 to 1365) Kihlberg,B.M., Sjoberg,U., Kasterm,W. and Bjorck,L. Protein LG: a hybrid molecule with unique immunoglobulin binding properties J. Biol. Chem. 267 (35), 25583-25588 (1992) 93094283 GenBank staff at the National Library of Medicine created this entry [NCBI gidsq 120302] from the original journal article. This sequence comes from Fig. 2. location/Qualifiers 1..987				
FEATURES					
SOURCE					

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BASE COUNT
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DB	716	TTAAATATTTAAATTTCTGCAAAAAGAA-----AAACACCAAAAGAACCCAAAAGAAAG	769	
QY	62	ttacaatcaagaattacttaactctctgacagatggaagaatacaaaacagcaagattccaag	121	
DB	770	TTACATATTAAACCAAACTTAATCTATGCGATGTGAAAAAAGCTCAAAACAGCAGAGTTCCAAG	829	
QY	122	gaacatttgaagaagaacagaacagaaagcttacaagatatgcagacttatagaacaagttaa	181	
DB	830	GAACATTTCGAACAGCAACAGCAAGCATTAACGATTAACCTCATTATTATGCAAAAAGAA	889	
QY	182	atgagcaatatacagacagactlagaagatgctgcgaacaccatatgaaacattaaattgcgt	241	
DB	890	ATGCTAAATATATACAGCAGACTTAGAAGATGCTGATATACCTATTTATATTAGATTTCAG	949	
QY	242	gaaataaa	249	
DB	950	GTTACGAAA	957	

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BASE COUNT      1141 a       412 c       490 g       614 t
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Query Match          72.8%; Score 181.2; DB 1; Length 2657;
Best local Similarity 86.3%; Pred. No. 3.9e-24;
Matches 214; Conservative 0; Mismatches 28; Indels 6; Gaps 1;

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QY     2   tgaacattaattgcttggaaagaacaaccagaaacccagaaagcaaaccaagaagaag 61
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QY     62   ttacaatcaagttaacttaactcctttggaagatgtgaagatacaagaaggagaattccaag 121
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1286 TTACTATTAAAGCAAACCTTAATCTATGTGAGATGGAAAAAATCTCAANACGACAGTTCAAAG 1345
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QY     122   gaacattggaagaagcaacagcagaagcttcacagatatgcagacttattagcaaaagtaa 181
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QY     182   atggcgcaatatacacgacagacttagaagatggttggaaccaatagaaacttaattgctg 241
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Db    1406 ATGGTAAATATAACGACAGACTTAGAAGATGGTGATACACTATTATATTAGATTGCCAG 1465
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY     242   gaaaataaa 249
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1466 GTAAAGAAA 1473

RESULT 11
AX022441 AX022441 548 bp DNA linear PAT 07-SEP-2000
LOCUS Sequence 1 from Patent EP035612.
DEFINITION
ACCESSION AX022441
VERSION AX022441.1 GI:10046055
KEYWORDS
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BASE COUNT	184 a	118 c	129 g	117 t
ORIGIN				
Query Match	44.1%	Score 109.8;	DB 6;	Length 548;
Best Local Similarity	68.0%;	Pred. No. 5.7e-11;		
Matches 153;	Conservative 0;	Mismatches 72;	Indels 0;	Gaps 0;
Db	25	gaacaccagaagaacccagaagaacccaagaagaagatgataatcaatgaagtaacttaac 84		
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Db	52	GTAGCGCAGCGCGCTCCGAAGATATACACGAGAGAGTACAGATCAAAAGCGACCTGATC 111		
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Db	85	tttgcagatggaagaatatacaacagcagaattcaaaaggaacatttgaagaagcaacaga 144		
	1			
Db	112	TTTGCAAATGTGTACACACCAAACTGCACAATTTCAAAAGGTACTTCGAAAAGCGACCTCG 171		
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Qy	145	gaacttcagatgatactgacagattatgcaaaagttaaatgacgaatatagacagactta 204		
	1			
Db	172	GAACTTATGCGGTATGACGATCTTTGAAGAAAGACAAATGGTGANTATATCTGTATGATGT 231		
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Qy	205	gaagatggtggaacacatatgaacattaacttctgtggaataa 249		
	1			
Db	232	GCAGATAAGAGTTACACCCCTGAACATCAATTCGGGGTAAAGAA 276		
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RESULT 13				
AX034619				
LOCUS	AX034619	548 bp	DNA	Linear
DEFINITION	Sequence 1 from Patent WO915563.			PAT 22-SEP-2000
ACCESSION	AX034619			
VERSION	AX034619.1	GI:10303209		
KEYWORDS				
SOURCE	Finegoldia magna.			
ORGANISM	Finegoldia magna			
REFERENCE	Bacteria: Firmicutes; Bacillus/Clostridium group; Clostridiaceae; Finegoldia.			
AUTHORS	1 (bases 1 to 548)			
TITLE	Koentgen, F., Suess, G.M., Tarlinton, D.M. and Treutlein, H.R.			
JOURNAL	Catalytic antibodies and a method of producing same			
	Patent: WO 911563-A 1 01-Apr-1999;			
	KOENTGEN FRANK (AU) ; AMRAD OPERATIONS PTY LTD (AU) ; SUESS			
	GABRIELE MARIA (AU) ; TARLINTON DAVID MATTHEW (AU) ; TREUTLEIN			
	HERBERT RUDOLF (AU)			
FEATURES	Location/Qualifiers			
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	/db_xref="GI:10303210"			
	/translation="MKRTATAIALAGFATVAQAAPKDNTEETIKANLIIFANGSTO			
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	DNGEYTVADVADKGTLLINIKFAG"			
BASE COUNT	184 a	118 c	129 g	117 t
ORIGIN				
Query Match	44.1%	Score 109.8;	DB 6;	Length 548;
Best Local Similarity	68.0%;	Pred. No. 5.7e-11;		
Matches 153;	Conservative 0;	Mismatches 72;	Indels 0;	Gaps 0;
Db	25	gaacaccagaagaacccagaagaacccaagaagaagatgataatcaatgaagtaacttaac 84		
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Db	85	tttgcagatggaagaatatacaacagcagaattcaaaaggaacatttgaagaagcaacaga 144		
	1			
Db	112	TTTGCAAATGTGTACACACCAAACTGCACAATTTCAAAAGGTACTTCGAAAAGCGACCTCG 171		
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Qy	145	gaacttcagatgatactgacagattatgcaaaagttaaatgacgaatatagacagactta 204		
	1			
Db	172	GAACTTATGCGGTATGACGATCTTTGAAGAAAGACAAATGGTGANTATATCTGTATGATGT 231		
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Qy	205	gaagatggtggaacacatatgaacattaacttctgtggaataa 249		
	1			
Db	232	GCAGATAAGAGTTACACCCCTGAACATCAATTCGGGGTAAAGAA 276		
	1			

OY	145	gaacttacagatatgcagaacctatttagcgaagaataatgccaatatccagacagactta	204
Db	172	GAACTTATGCGGTATGCAGACTACTTTGAAGAACAACATAITGGTAGATATACTGTAAGTGTT	231
OY	205	gaagtgttgaaaccatalatgaacatlaaatlctgtcggaanaataa	249
Db	232	GCAGATTAAAGSTTACACCCTGACCATCAAAATTCCGGGATTAAGAA	276
RESULT	14		
AX022452		539 bp	DNA
LOCUS:	Sequence 12 from Patent EP0935612.		linear
DEFINITION	AX022452		PAT 07-SEP-2000
ACCESSION	AX022452		
VERSION	AX022452.1	GI:10046066	
KEYWORDS			
SOURCE	unidentified.		
ORGANISM	unclassified.		
REFERENCE	1 (bases 1 to 539)		
AUTHORS	Koentgen,F., Sness,G.M., Tarlington,D.M. and Treutlein,H.R.		
TITLE	Precursors of catalytic antibodies		
JOURNAL	Patent: EP 0935612-A 12 18-AUG-1999;		
FEATURES	AMRD OPERATIONS Pty LTD (AU)		
source	Location/Qualifiers		
CDS	1..539		
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BASE COUNT	161 a . 116 c . 130 g . 112 t		
ORIGIN			
Query Match	43.0% Score 107; DB 6; Length 539;		
Best Local Similarity	.71.8%; Pred. No. 1.8e-10;		
Matches 140; Conservative	0; Mismatches 55; Indels	0; Gaps	0;
OY	55	gaagaagtacatcaagaattaacttaacttcitcgagatggagaatatacaacacagcagaa	114
Db	34	GAAGAAGTCACGATTCACAAAGCAGAACCTGATCTTTGCCAATGTAAGCACAACAACTCGAGAA	93
OY	115	tccaaggaaacatttgaagaagcaaacagagaagcttacagatatgcagactttaagca	174
Db	94	TTCAAAGGTACCTTCACAAAAGCGACCTCGAAGCTTATGCCGTATGCAGATACCTTTGAAG	153
OY	175	aaaagtaaattggcgaatatcacagagacttagaagatgytgtgaacacatatgaacatltaa	234
Db	154	AAAGACAAATGCTAAATATACTGTAGATGTTTTCGACGATTAAGGTTACACCCCTGAACATCAAA	213
OY	235	tttgcctggaataataa	249
Db	214	TTCCGCGGTAAAGAA	228
RESULT	15		
AX030809		539 bp	DNA
LOCUS:	Sequence 12 from Patent US6043069.		linear
DEFINITION	AX030809		PAT 20-SEP-2000
ACCESSION	AX030809		
VERSION	AX030809.1	GI:10278307	
KEYWORDS			
SOURCE	unidentified.		
ORGANISM	unclassified.		

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REFERENCE 1 (bases 1 to 539)
AUTHORS Koentgen, F., Suesse, G.M., Tarlinton, D.M. and Treutlein, H.R.
TITLE Catalytic antibodies and a method of producing same
JOURNAL Patent: US 6043069-A 12-28-MAR-2000;
AMRAD OPERATIONS PTY LTD (AU)
FEATURES
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        location/Qualifiers
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                NIKRAGRESAMRHPDQGS"
BASE COUNT 181 a 116 c 130 g 112 t
ORIGIN
Query Match 43.0%; Score 107; DB 6; Length 539;
Best Local Similarity 71.8%; Pred. No. 1.8e-10;
Matches 140; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY 55 gaagaagttacaatcaagaagttacttaattcttgcagatggaagaatataaacaagcagaa 114
Db 34 GAAGAAGTCAAGTCACGATCAAAAGCAACCGATCTTTGCCAAATGGTAGCACACAAACTGCAGAA 93
QY 115 ttcaagggaacatttgaagaagcaacagcagaagcttacagatatgcagactattagca 174
Db 94 TTCAAGGATACCTTCGAAAAAGCGACCTCGAAGCTTATGCGTATGCATATCTTTGAGG 153
QY 175 aaagtaaatgycgaatalaacaagcagacttagaagatggtggaaccatatgaacattaa 234
Db 154 AAAGACAATGTGTAATATACTGTAGATGTTGCAGATTAAGGTTACACCTGAAACATCAAA 213
QY 235 ttgtcgtgaaataa 249
Db 214 TTGCGGGGTAAAGAA 228

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